

FIG. 2

INHIBITION OF natIL-12-INDUCED PHA BLAST
PROLIFERATION BY ANTI-IL-12 mAbs

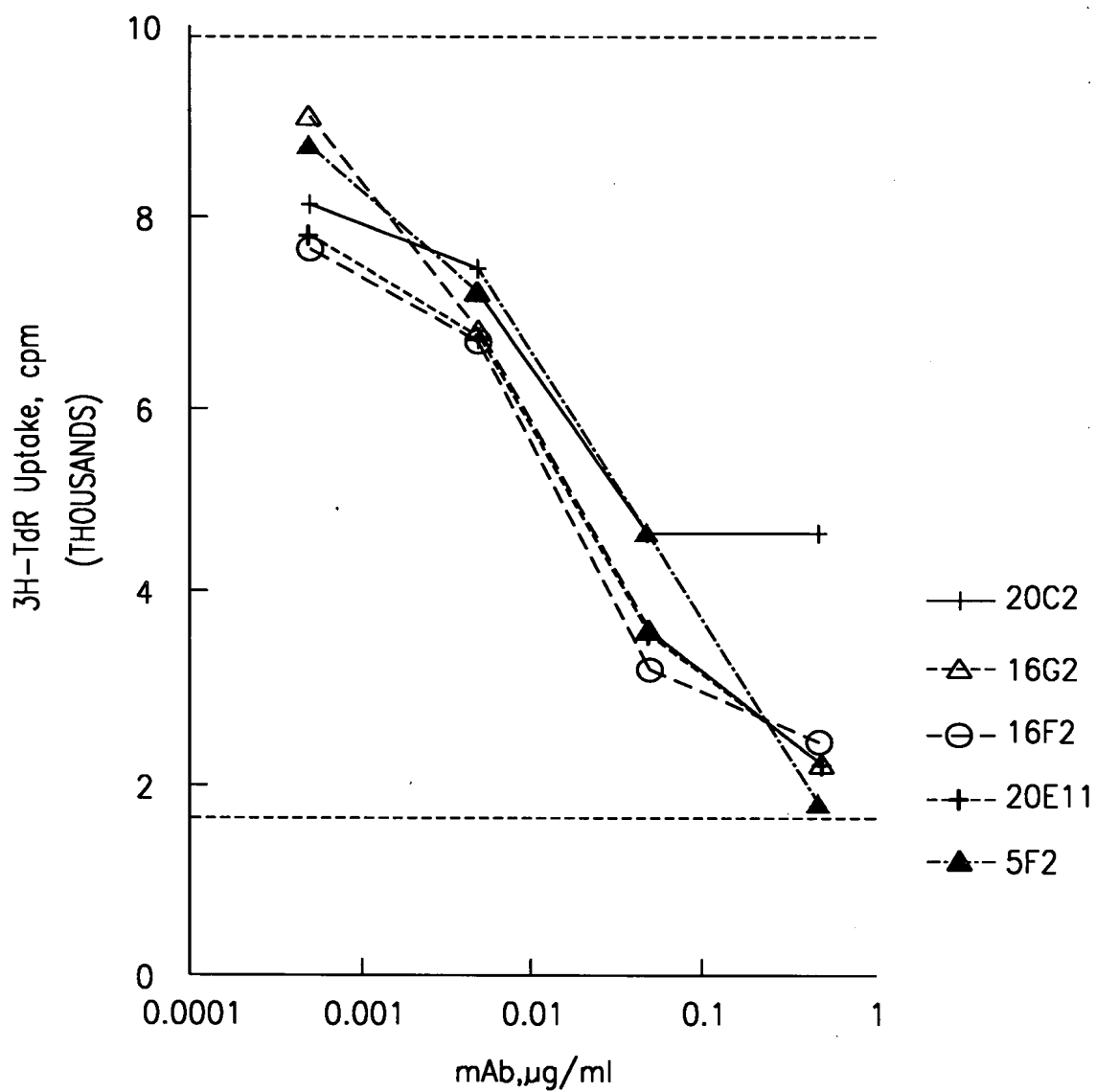


FIG. 3

INHIBITION OF RHESUS IL-12-INDUCED PHA BLAST
PROLIFERATION BY ANTI-IL-12 mAbs

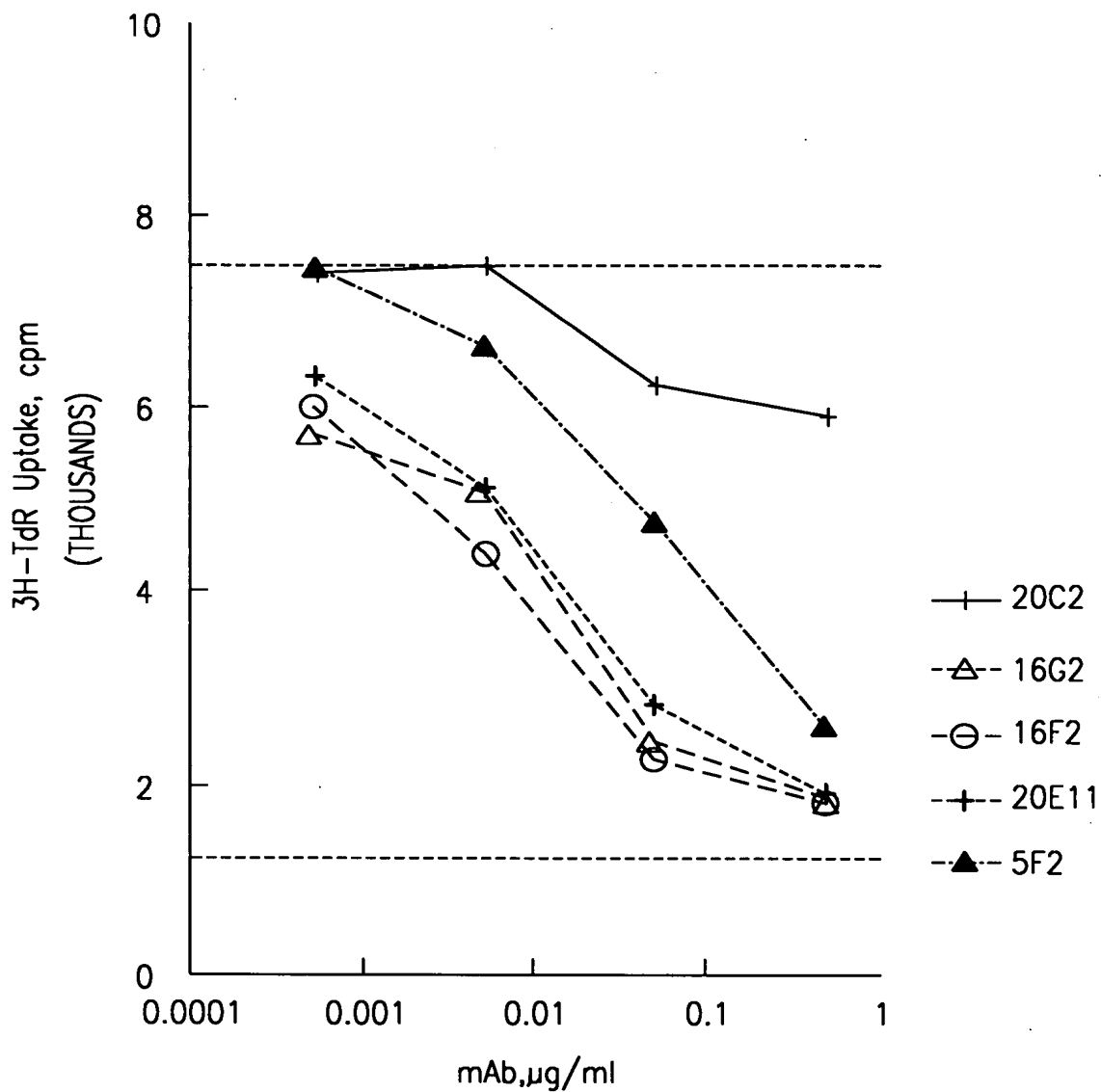


FIG. 4

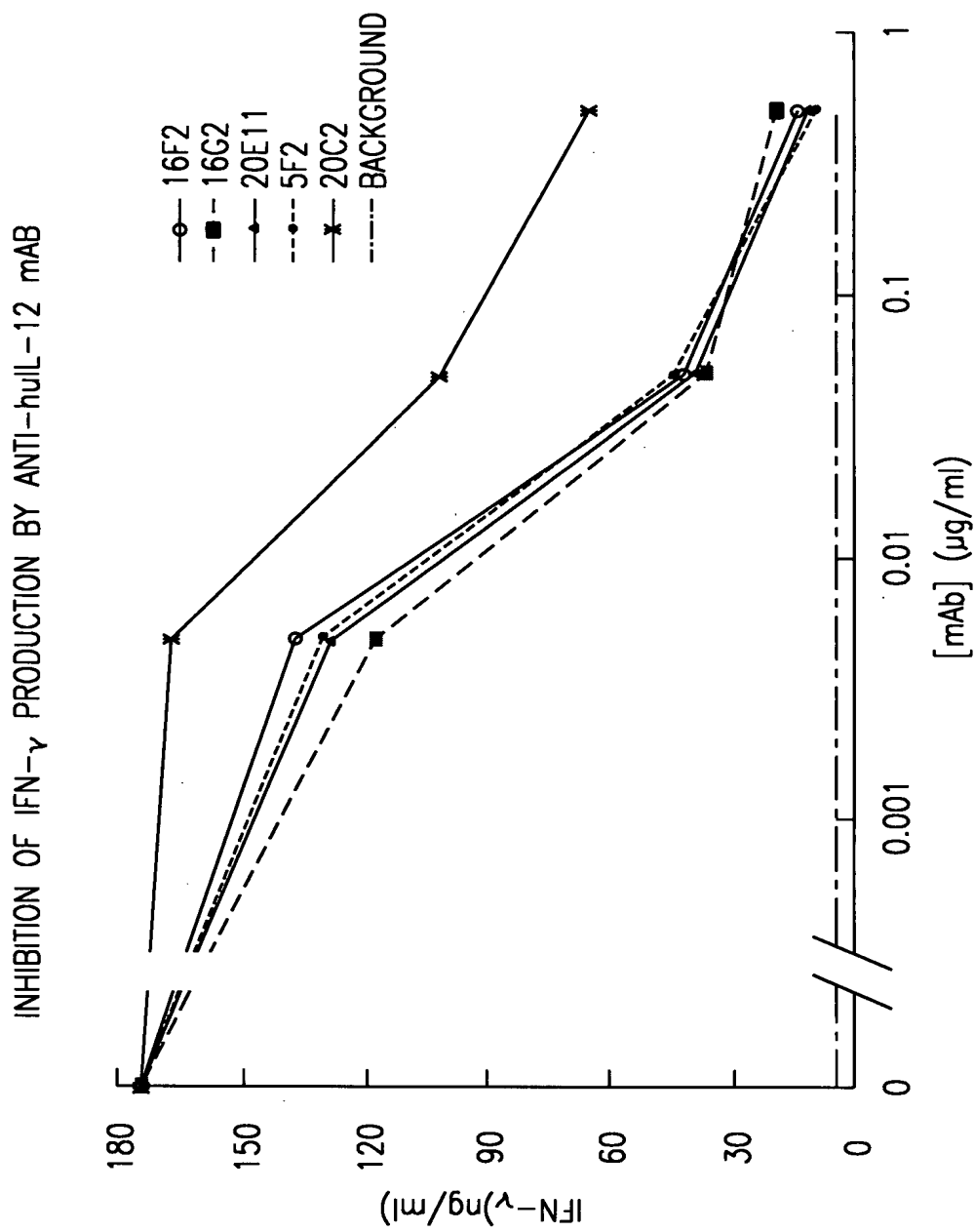


FIG. 5

16G2 HEAVY CHAIN VARIABLE REGION

27 54
 CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC ACC
 GAC CTC CTC AGT CCT GGA TCG GAG CAC TT GGA AGA GTC TGA GAC AGG GAG TGG
 Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr

81 108
 TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG ATC CGG AAA
 ACA AGA CAG TGA CCG CTG AGG TAG TGG TCA CCA ATG ACC TTG ACC TAG GCC TT
 Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp Ile Arg Lys

135 162
 TTC CCA GG AAT AAA TT GAG TAC ATG GGA TTC ATA AGT TAT AGT GGT AGC ATC
 AAG GGT CCC TTA TT AAA CTC ATG TAC CCT AAG ATA TCA ATA TCA CCA TCG TGA
 Ph Pro Gly Asn Lys Ph Glu Tyr MET Gly Phe Ile Ser Tyr Ser Gly Ser Thr

189 216
 TAC AAT ATT CCA TCT CTC AAA AAT CGA GTC TCC ATC ACT CGA GAC ACA TCC AAT
 ATG TTA TTA GGT AGA GAG TT TTA GCT CAG AGG TAG TGA GCT CTG TGT AGG TTA
Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val Ser Ile Thr Arg Asp Thr Ser Asn

243 270
 AAC CAG TAC TAC CTG CAG TTG AGT TCT GTG ACT ACT GAG GAC TCA GCC ACA TAT
 TTG GTC ATG ATG GAC GTC AAC TCA AAG CAC TGA TGA CTC CTG AGT CGG TGT ATA
 Asn Gln Tyr Tyr Leu Gln Leu Ser Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr

297
 TAC TGT GCA AGA TCT TCG GAT GCT TTG GAC TAC TGG GGC CGA GG ACC ACG
 ATG ACA CGT TCT AGA AGC CTA CGA AAC CTG ATG ACC CCG CGT CCC TGG TGC
 Tyr Cys Ala Arg Ser Ser Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr

FIG. 6

20E11 HEAVY CHAIN VARIABLE REGION

27 54
 GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC ACC TGT
 CTC CTC AGT CCT GGA TCG GAG CAC TT GGA AGA GTC TGA GAC AGG GAG TGG ACA
 Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys
 81 108
 TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG ATC CGG AAA TTC
 AGA CAG TGA CCG CTG AGG TAG TGG TCA CCA ATG ACC TTG ACC TAG GCC TT AAG
 Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp Ile Arg Lys Phe
 135 162
 CCA GAT AAT ACA CTT GAG TAC ATG GGA TAC ATA AGT TAC AGT GGT AGT ACT TAC
 GGT CTA TTA TGT GAA CTC ATG TAC CCT ATG TAT TCA ATG TCA CCA TCA TGA TGA
 Pro Asp Asn Thr Leu Glu Tyr MET Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Tyr
 189 216
 TAC AAT CCA TCT CTC AGA AGT CGA ATC TCC ATC ACT CGA GAC ACA TCC AAG AAC
 ATG TTA GGT AGA GAG TCT TCA GCT TAG AGG TAG TGA GCT CTG TGT AGG TTC TTG
Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn
 243 270
 CGA TAC TCC ATG CAG TTG AAT TCT GTG ACT ACT GAG GAC ACA GCC ACA TAT TAC
 GTC ATG AGG TAC GTC AAC TTA AGA CAC TGA TGA CTC CTG TGT CGG TGT ATA ATG
 Gln Tyr Ser MET Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr
 297
 TGT GCA AGA TCC TCG GAT GCT ATG GAC TAC TGG GGC GC
 ACA CGT TCT AGG AGC CTA CGA TAC CTG ATG ACC CCG CG
 Cys Ala Arg Ser Ser Asp Ala MET Asp Tyr Trp Gly

FIG. 7